

NIEHS Microarray User's Group  
Meeting:  
Factors Affecting RNA Quality  
Sample Submission Process

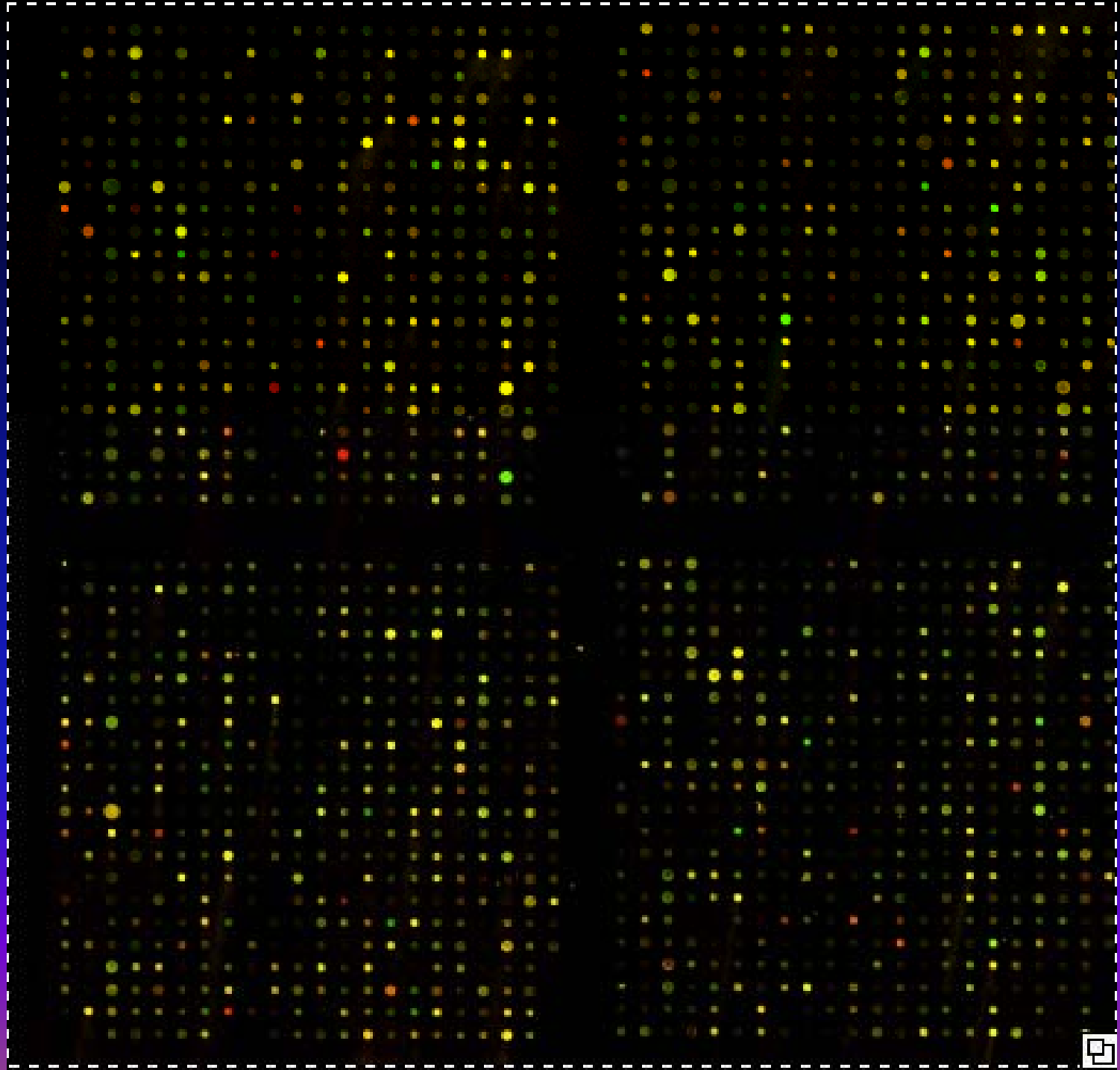
September 21, 2001  
Cindy Afshari, Ph.D.

# Outline

- How critical is RNA quality?
- Considerations for isolating high quality RNA
- Assessing RNA quality
- Submitting samples to the microarray lab

# How critical is RNA quality?

- RNA quality may be the biggest factor in determining the “picture perfect” hybridization
- RNA quality affects labeling efficiency
- RNA quality affects signal to noise ratio/background contribution



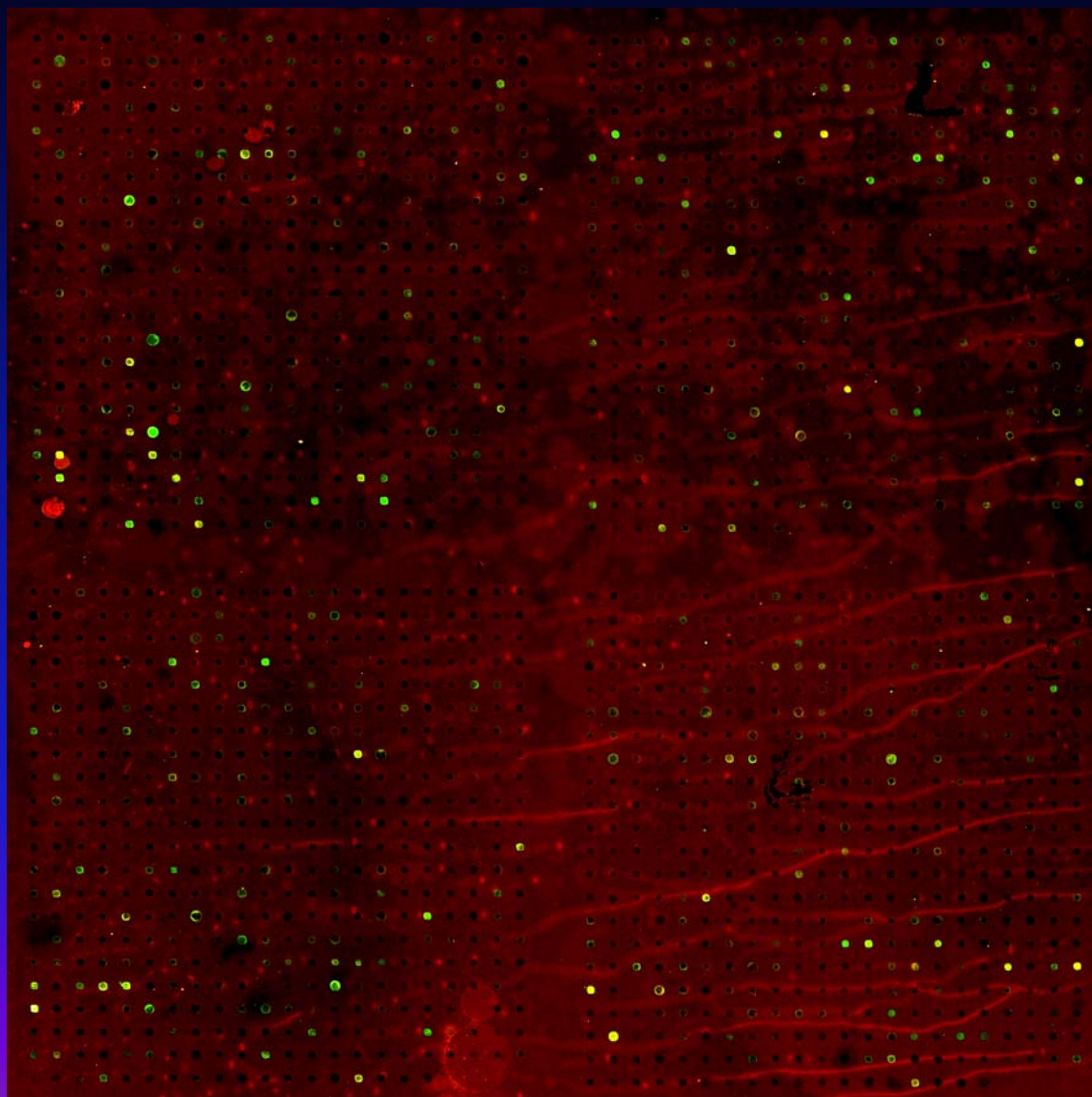
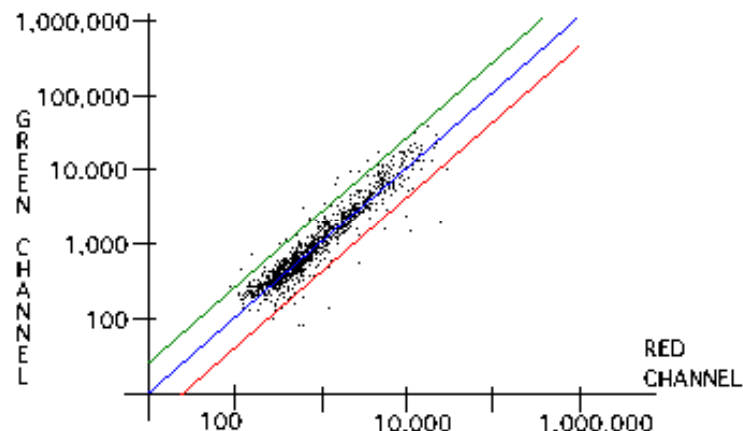


Image Name: **p30s13c3.tif**  
**p30s13c5rotflmarked**

☐ Histogram/ ☒ Scatter Plot



☒ Log Scale

☐ Calibrated Result

Confidence Level:	99.00	Intensity From:	1
Ratio Lower Limit:	0.38	Intensity To:	65535
Ratio Upper Limit:	2.45	Target Size From:	30

Data from:

- ☒ All targets
- ☐ Control targets

Calibration by:

- ☐ Internal Controls
- ☒ All targets
- ☐ Background

Calibration Method:

- ☒ Ratio Distribution
- ☐ Log-Normal

Refine Stats

CV = 0.218

M = 0.972

Exit

Refresh

Default Setting

Ratio Outliers

Update dataSheet

Equal Intensities

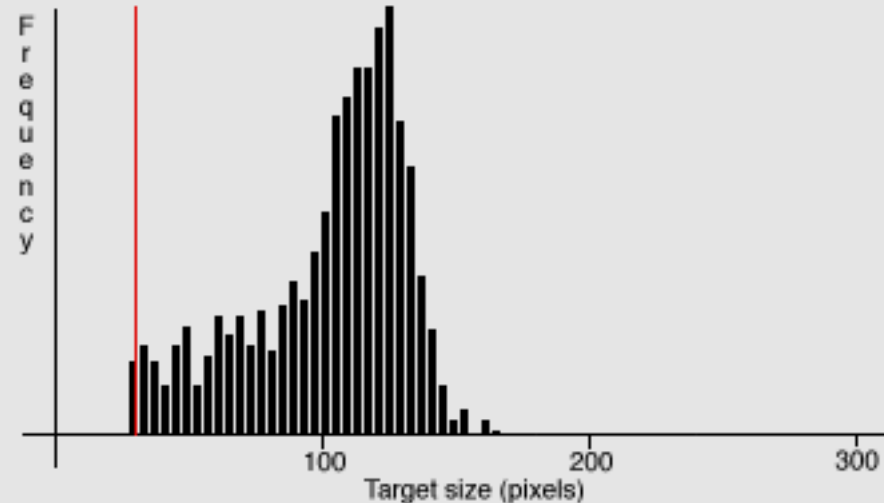
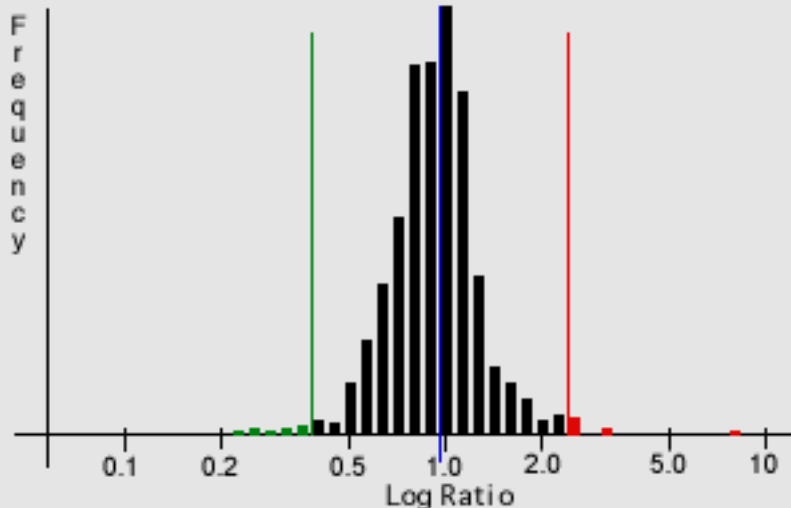
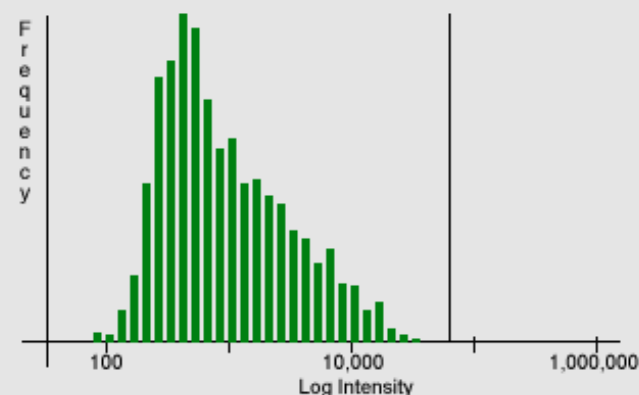
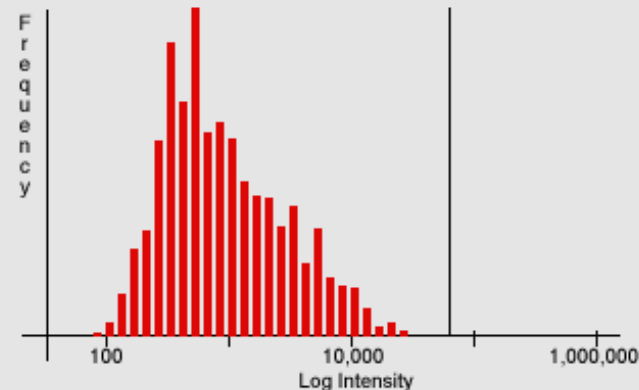
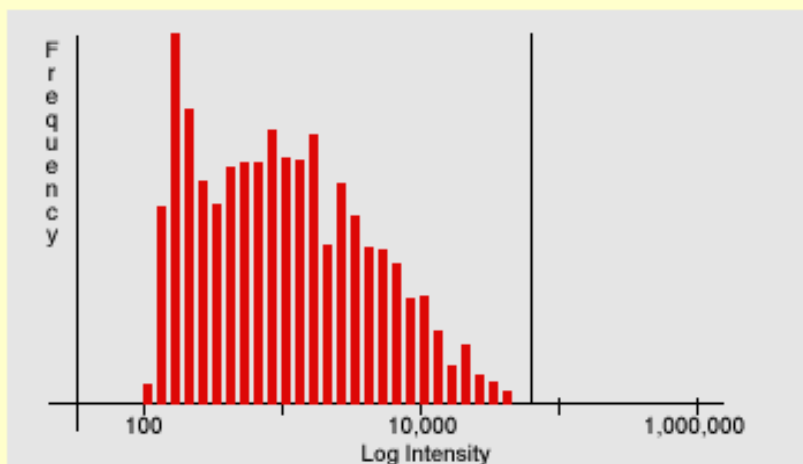


Image Name: **p21s85\_532\_flpmrk.IP**  
**p21s85\_635\_flp.IP**



☒ Log Scale

☐ Calibrated Result

Confidence Level:

99.00

Intensity From:

1

Ratio Lower Limit:

0.36

Intensity To:

65535

Ratio Upper Limit:

2.47

Target Size From:

30

☒ Histogram/ ☐ Scatter Plot

☐ Ratio

☒ Red channel

☐ Green channel

☐ Size

Data from:

☒ All targets

☐ Control targets

Calibration by:

☒ Internal Controls

☐ All targets

☐ Background

Calibration Method:

☒ Ratio Distribution

☐ Log-Normal

Refine Stats

CV = 0.223

M = 0.949

Default Setting

Ratio Outliers

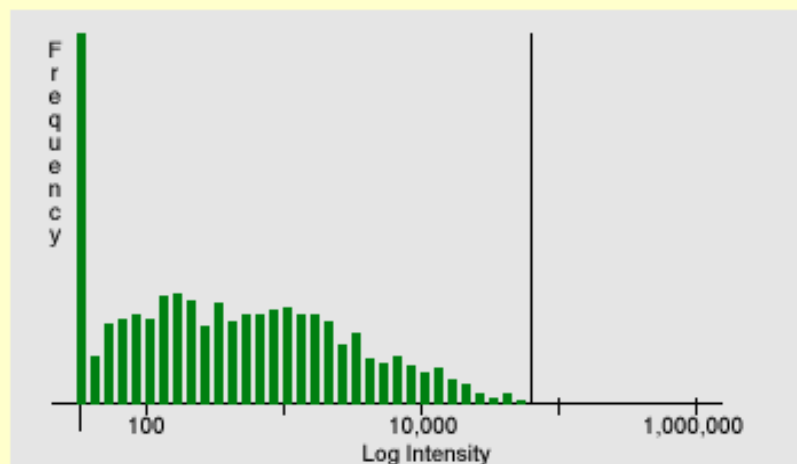
Update dataSheet

Equal Intensities

Exit

Refresh

Image Name: **p21s85\_532\_flpmrk.IP**  
**p21s85\_635\_flp.IP**



☒ Histogram/ ☐ Scatter Plot

- ☐ Ratio
- ☐ Red channel
- ☒ Green channel
- ☐ Size

Data from:

- ☒ All targets
- ☐ Control targets

Calibration by:

- ☒ Internal Controls
- ☐ All targets
- ☐ Background

Calibration Method:

- ☒ Ratio Distribution
- ☐ Log-Normal

☒ Log Scale

☐ Calibrated Result

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99.00

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0.36

Intensity To:

65535

Ratio Upper Limit:

2.47

Target Size From:

30

Refine Stats

CV = 0.223

M = 0.949

Default Setting

Ratio Outliers

Exit

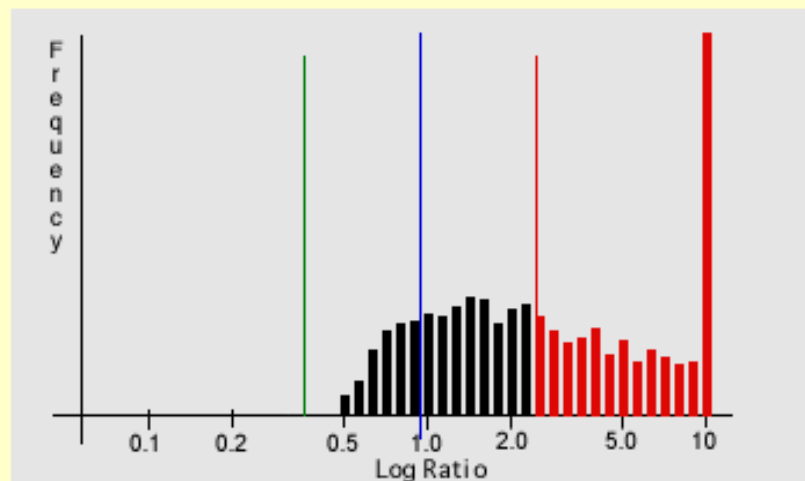
Refresh

Update dataSheet

Equal Intensities



Image Name: **p21s85\_532\_flpmrk.IP**  
**p21s85\_635\_flp.IP**



☒ Log Scale

☐ Calibrated Result

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99.00

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☒ Histogram/ ☐ Scatter Plot

☒ Ratio

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☐ Green channel

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☐ Control targets

Calibration by:

☒ Internal Controls

☐ All targets

☐ Background

Calibration Method:

☒ Ratio Distribution

☐ Log-Normal

Refine Stats

CV = 0.223

M = 0.949

Exit

Refresh

# Most commonly observed problems with RNA

- Degradation
- Quality/DNA contamination - gel
- Quantitation - concentration
- Low mRNA level/high rRNA
- pH/salt - some DEPC and sodium acetate
- Protein/glycolipid contamination

# Important Steps in RNA Isolation

- Tissue handling
- Tissue storage
- Tissue disruption
- RNA isolation
- RNA quantitation
- RNA storage

# Important Steps in RNA Isolation

- Tissue handling:
  - Culture or animal handling for harvest/necropsy
  - Freezing of cells/tissue
    - Size of tissue sample
    - Liquid nitrogen
    - RNA Later (Ambion)

# Important Steps in RNA Isolation

- Tissue storage:
  - Liquid nitrogen
  - RNA later
- Store until lysis buffer is added

# Important Steps in RNA Isolation

- Tissue disruption:
  - Sonicator, polytron, homogenizer
    - (see Julie Foley's presentation)
  - Poor disruption will affect amount and quality of yield

# Important Steps in RNA Isolation

- RNA isolation
  - Qiagen RNAeasy
  - Triazol or other methods
- Don't overload columns or volumes of solutions!!!!
- Be careful to reduce contamination from salts, ethanol, or organic solvents (phenol).

# Important Steps in RNA Isolation

- RNA quantitation
  - Consider a standard, commercial source to calibrate spectrophotometer
- RNA concentration



# Important Steps in RNA Isolation

- RNA storage:
  - -80 degrees
  - Move on dry ice
  - Aliquot if large amount
  - Thaw on ice

# Assessing RNA Quality

- OD 260/280 Ratio: 1.8- 2.0
- Ethidium bromide stained formaldehyde agarose gel
- Agilent Bioanalyzer



1

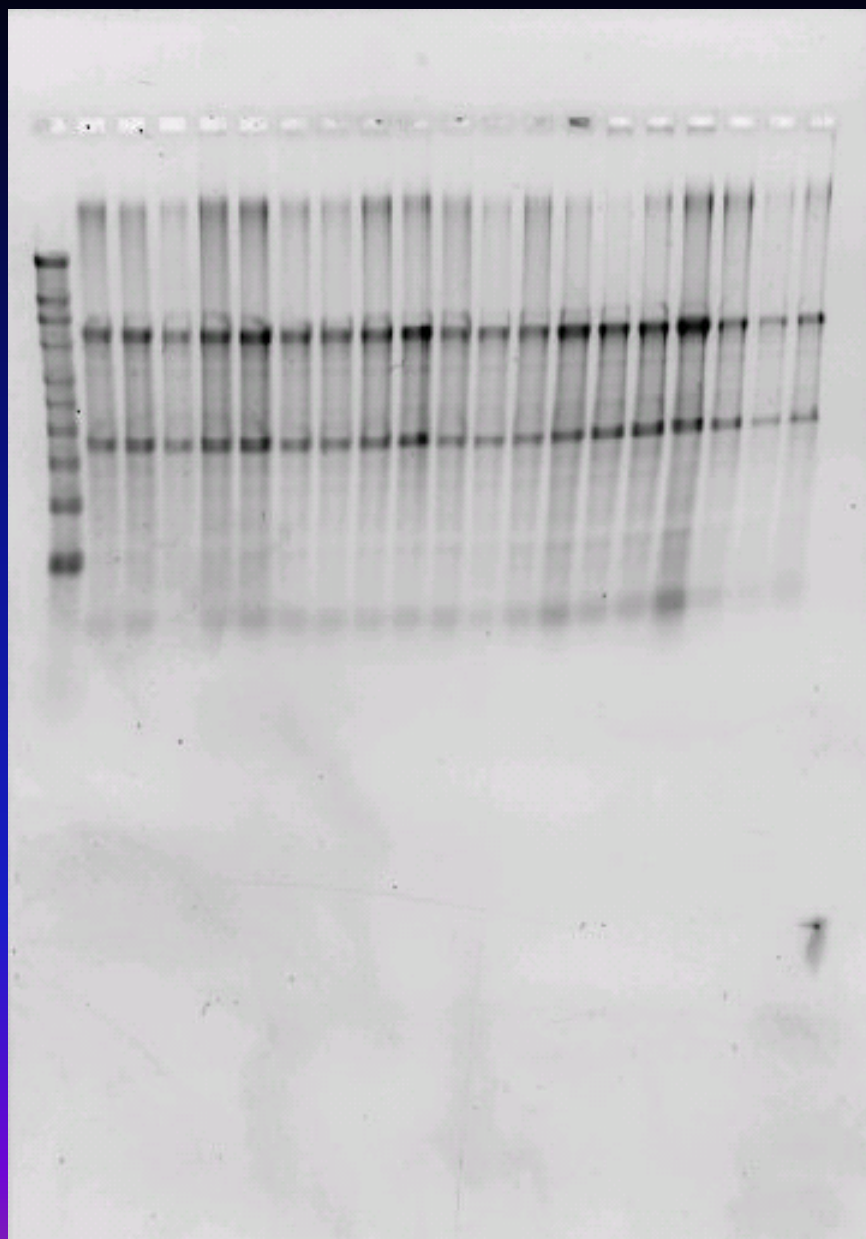
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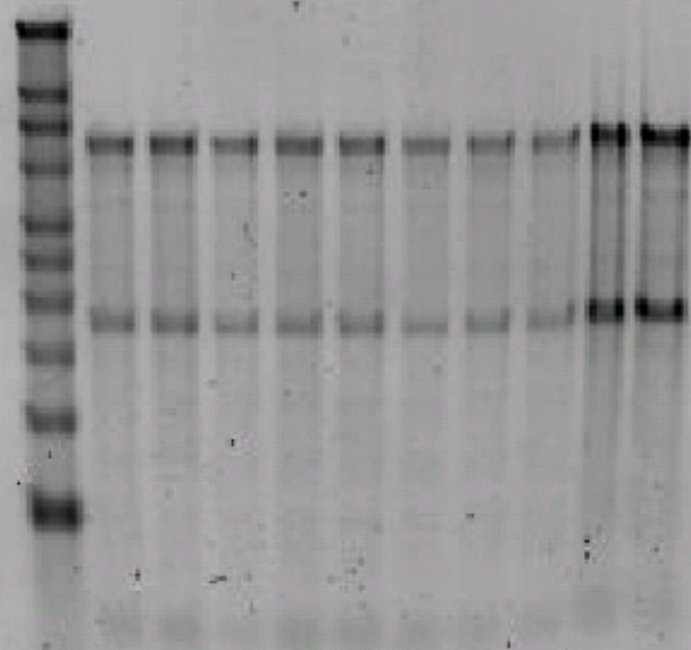
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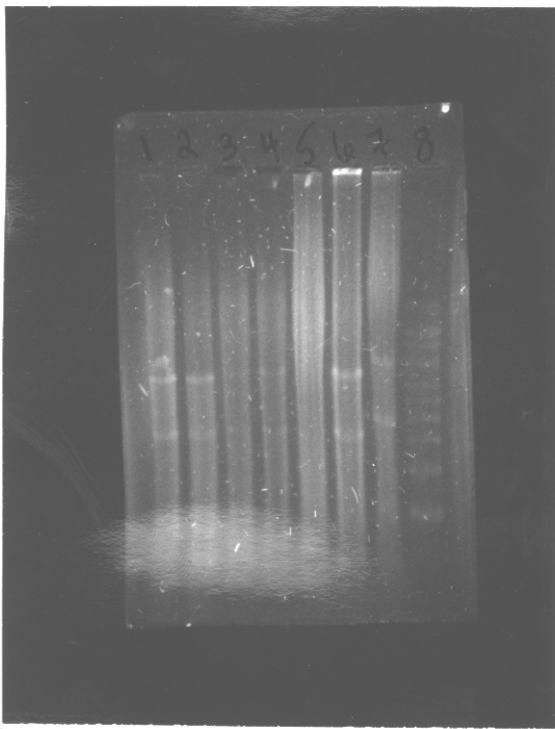


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5

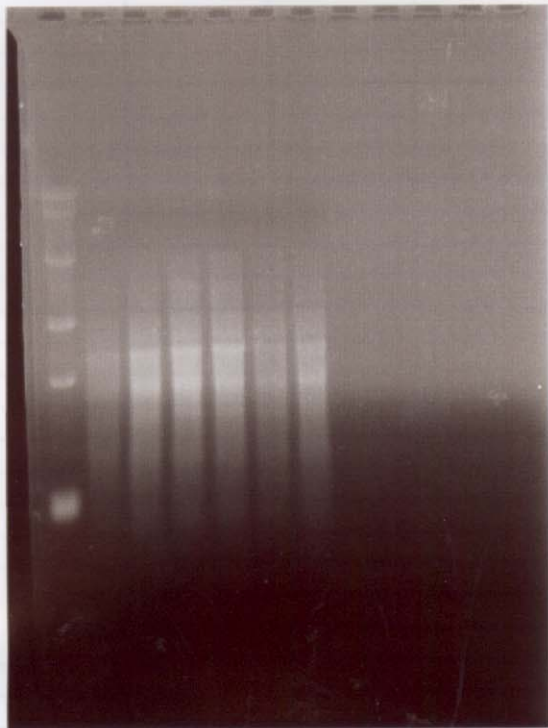






4 September 2001





Exp 12.08 Spc. B 14. W/255 G. 0.85 Dna 0.1 18. 2001 Time 18.37 Qd-2 14.00225 F 44 Standard

Lane

1

RNA ladder

2

BG-1 Control 2hr

3

BG-1 E2 2hr

4

BG-1 Control 6hr

5

BG-1 E2 6hr

6

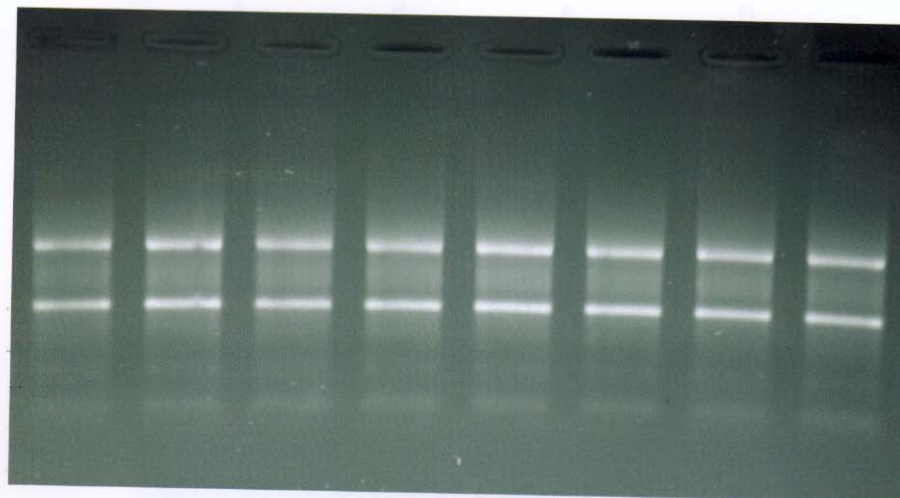
BG-1 Control 24hr

7

BG-1 E2 24hr



# RNA: Human Hearts 8/22/00



001a 001b 004a 004b 005a 005b 016a 016b

001 = Control 6/6/00  
004 = Failure 6/22/00  
005 = Failure 6/13/00  
016 = Failure 7/11/00



4 hr.

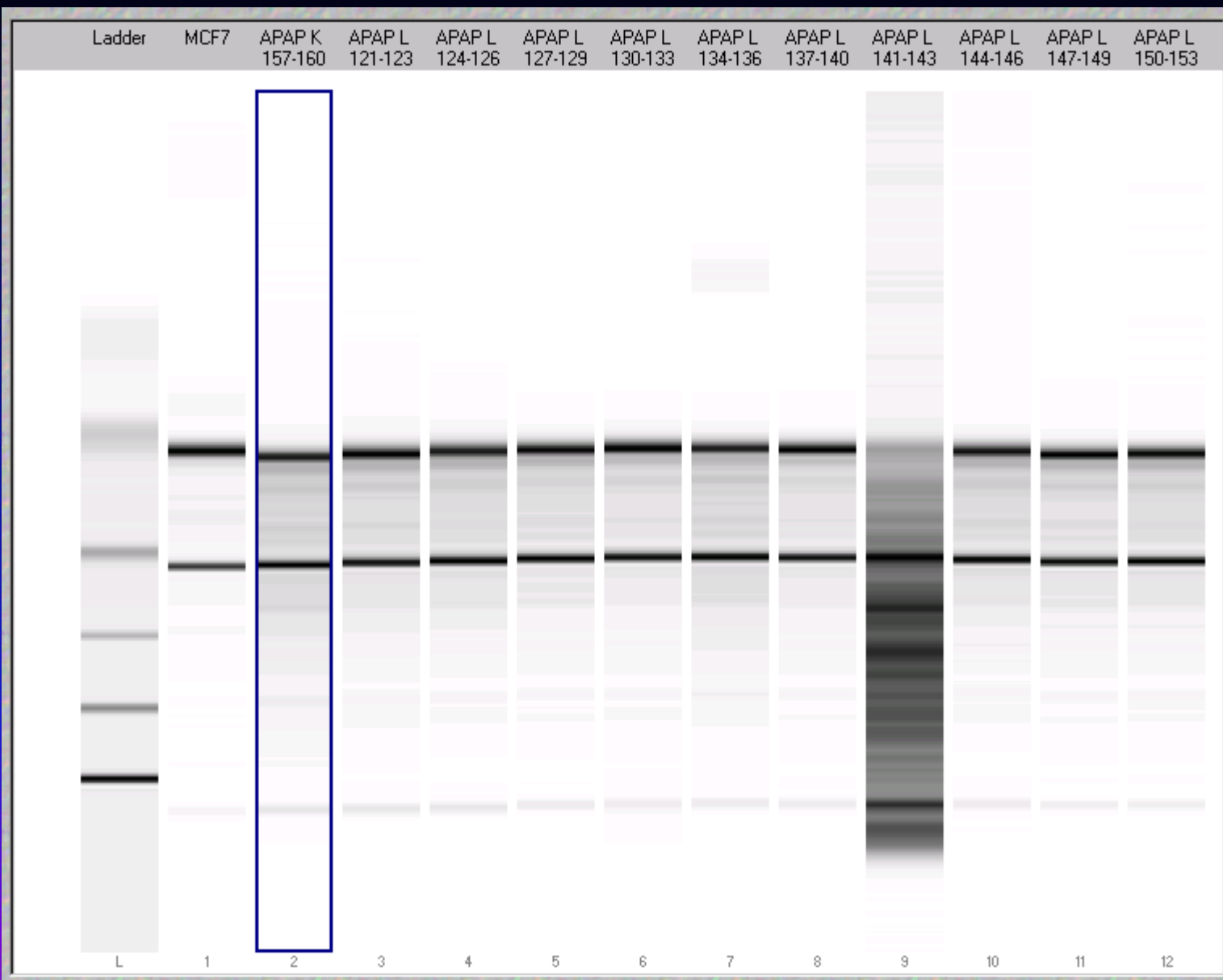
0, 0.2, 0.05, 0.05, 2.5, 2.5



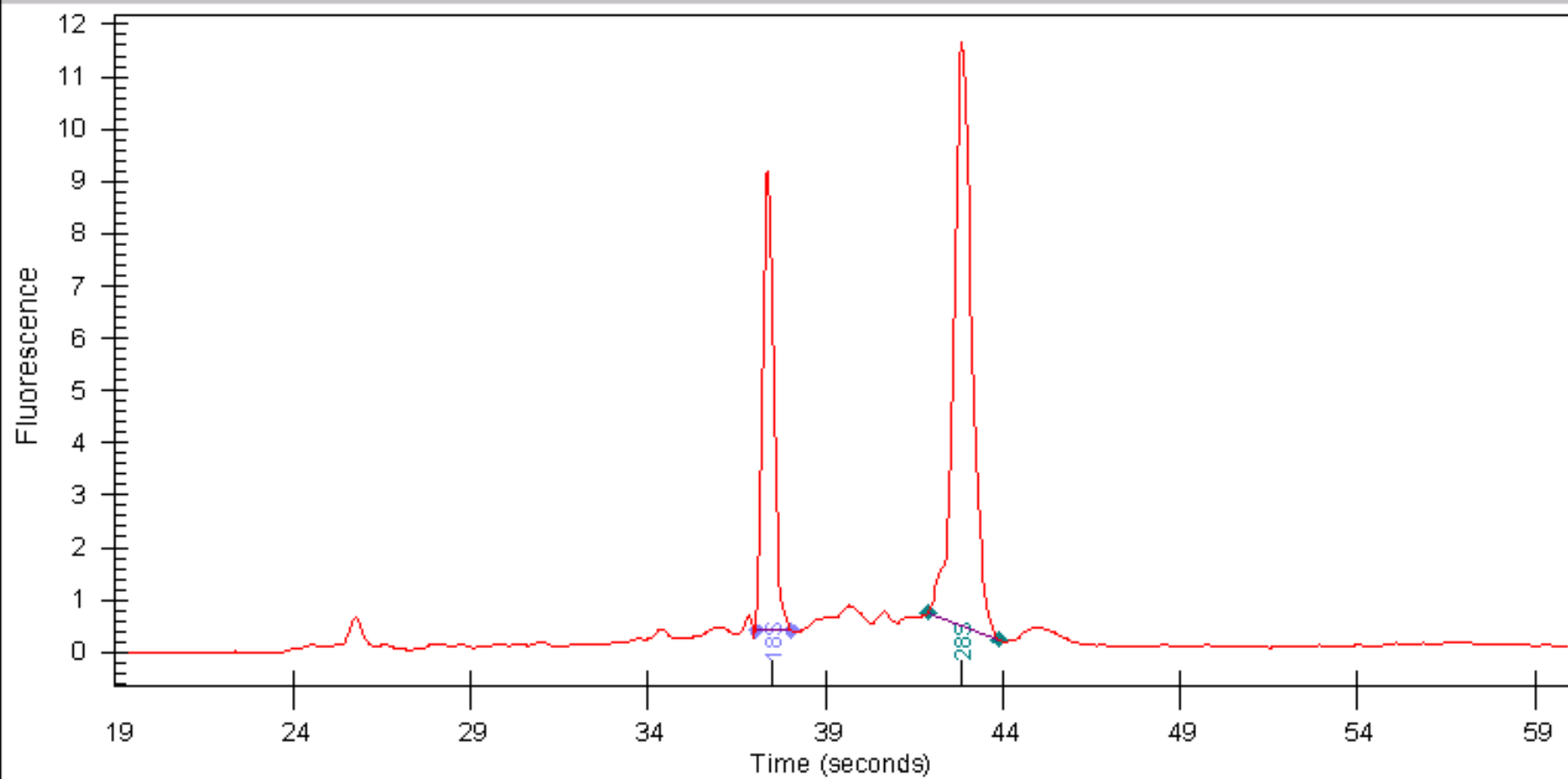
24 hr.

0, 0.2, 0.05, 0.05, 2.5, 2.5

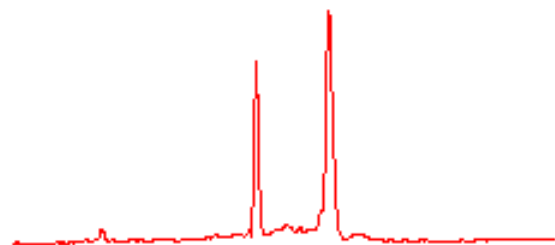
- RNA integrity
- diluted to 1 µg/µl
- 1 µg total per lane



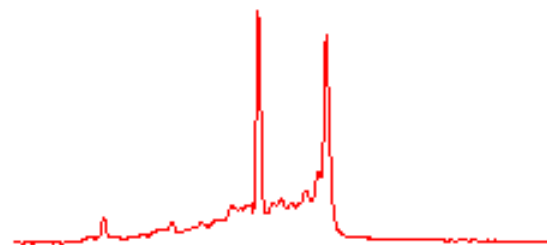
MCF7



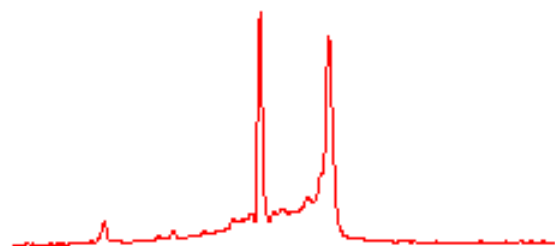
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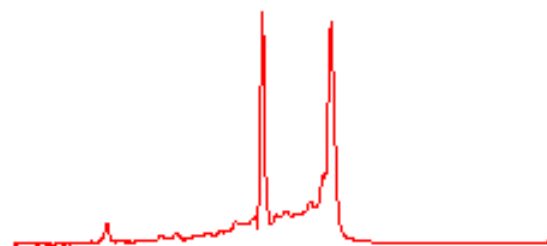
APAP K 157-160



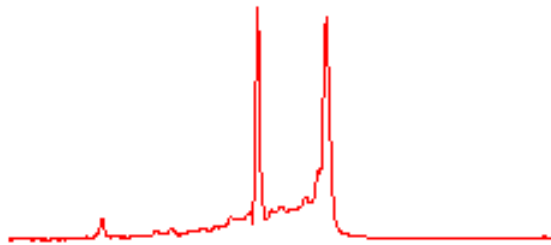
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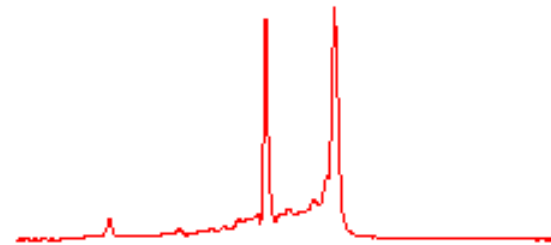
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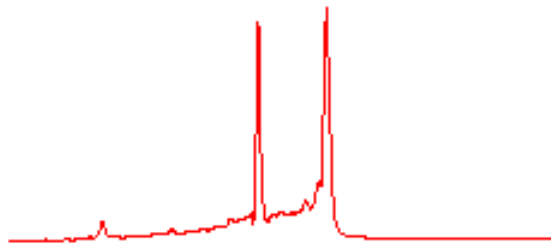
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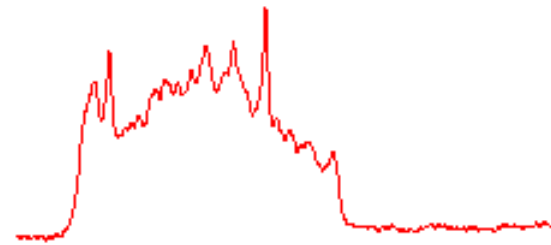
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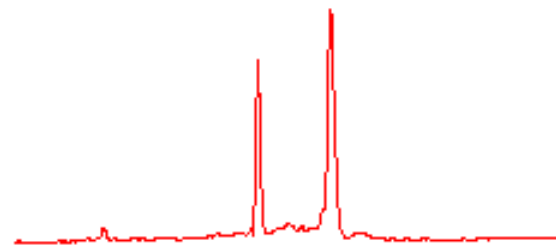
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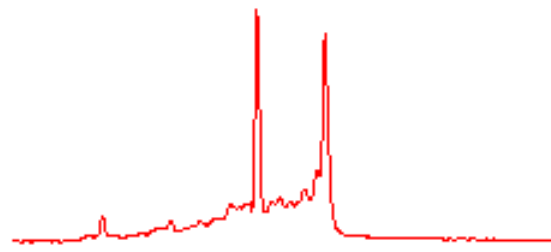
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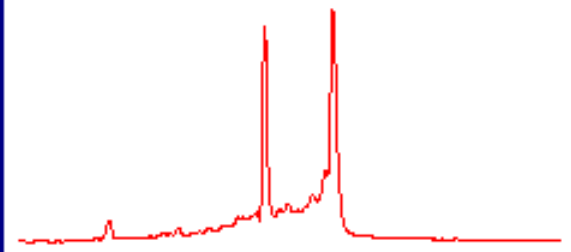
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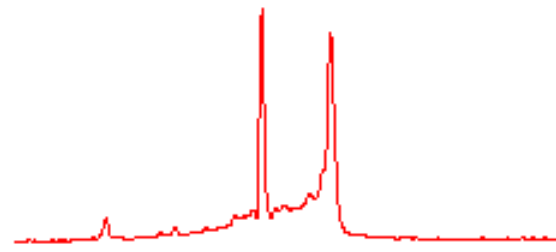
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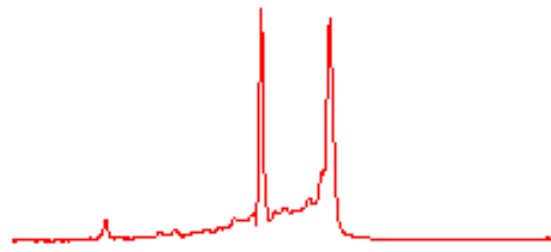
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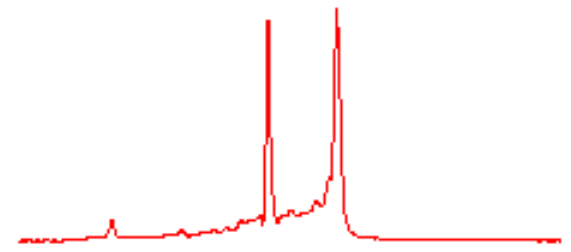
APAP L 124-126



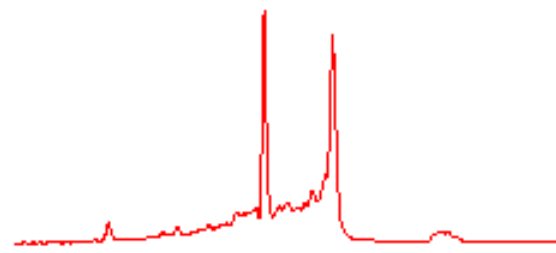
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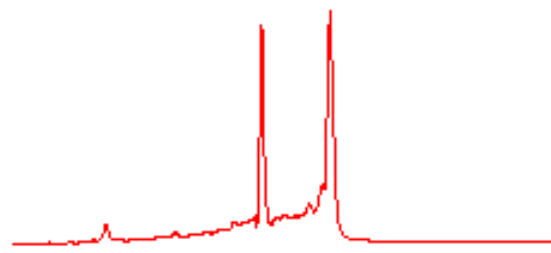
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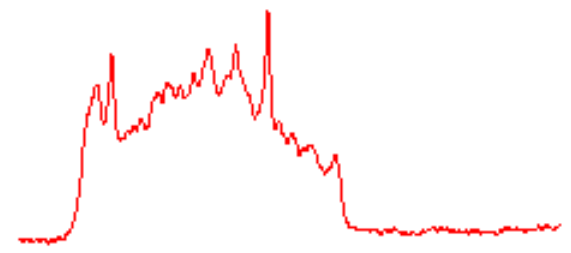
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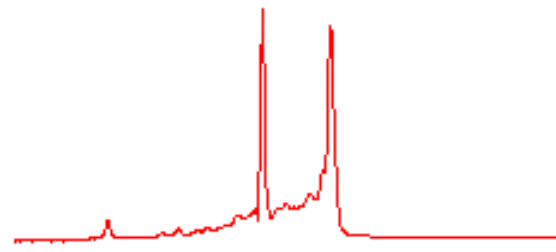
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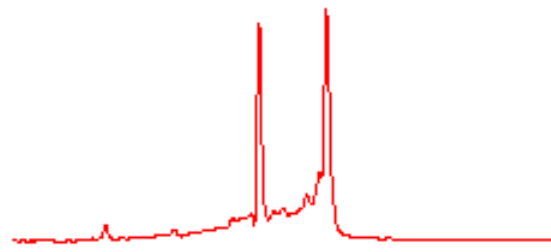
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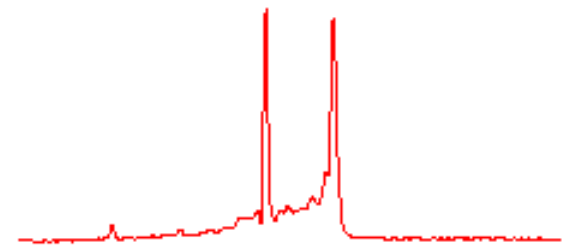
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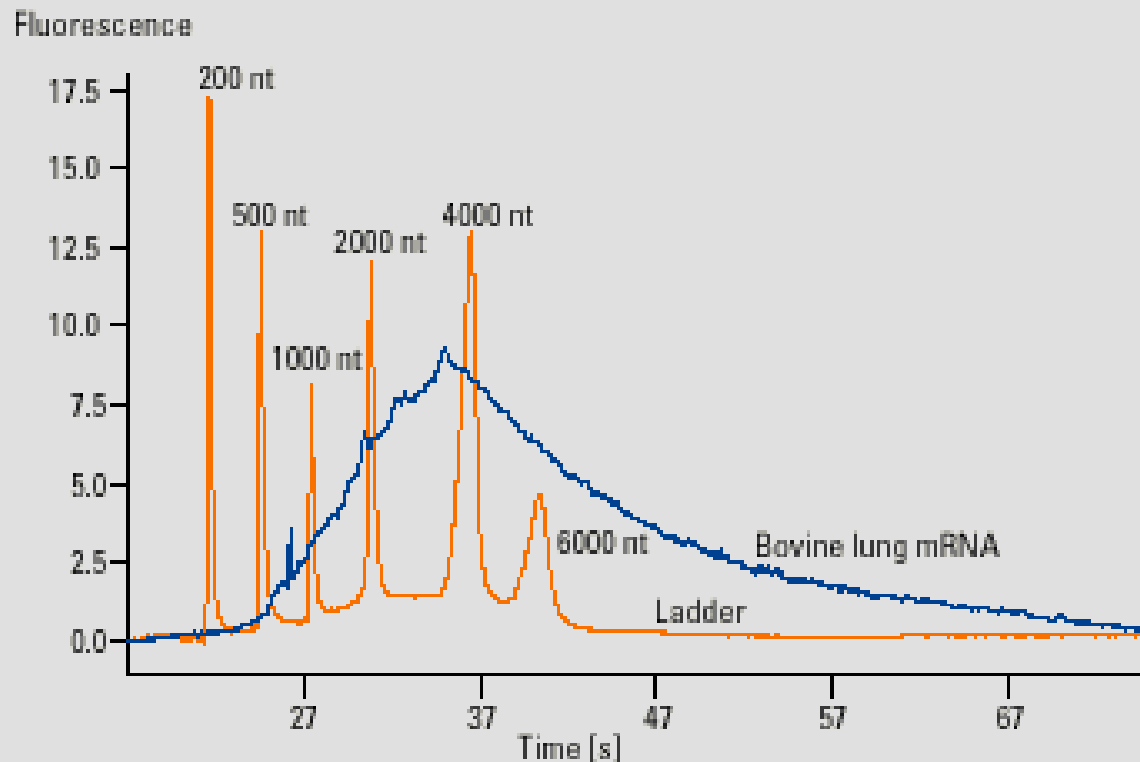


APAP L 147-149



APAP L 150-153



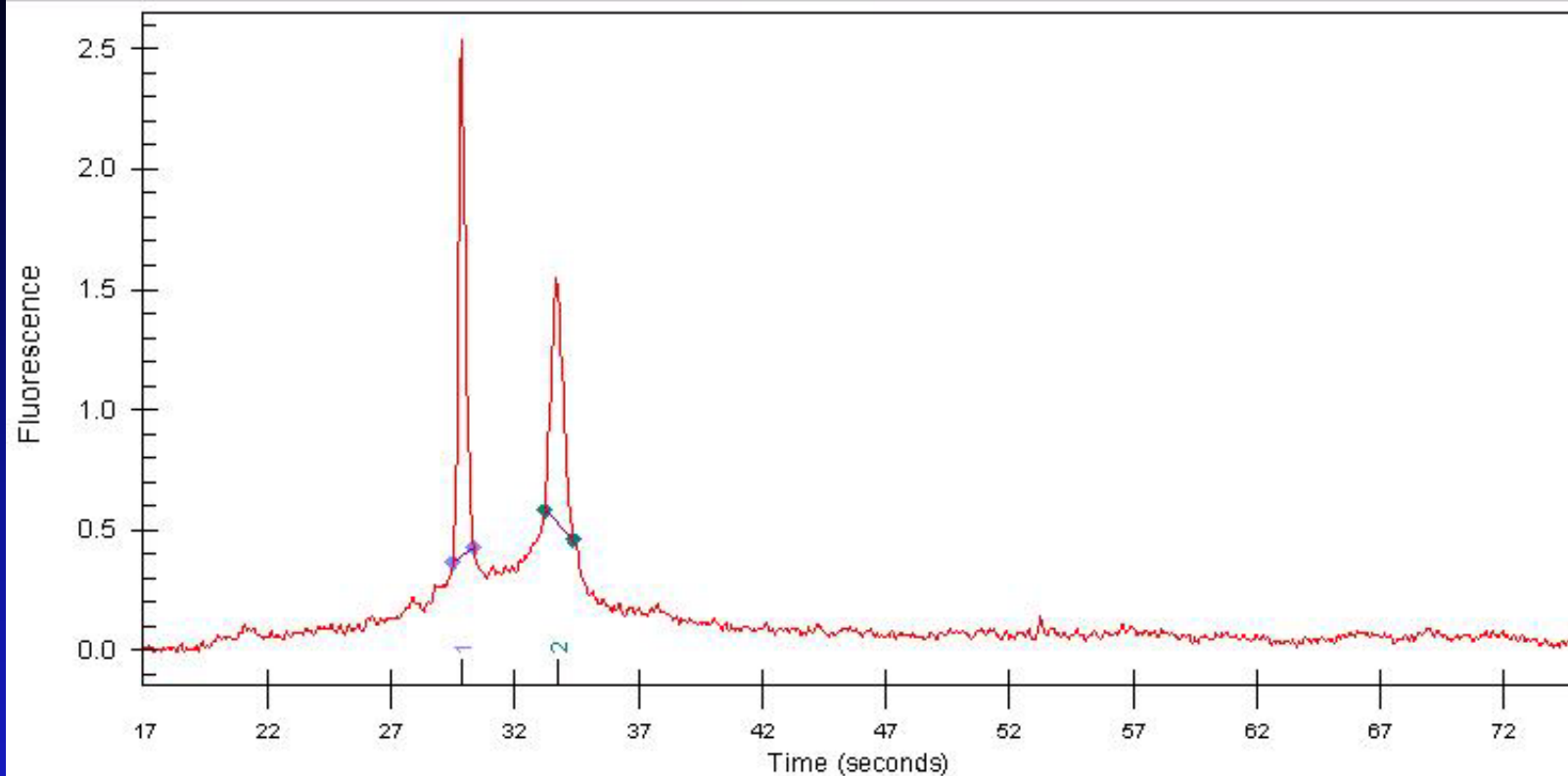


**Figure 1**

The relative amounts of transcripts falling in a certain size range can be estimated by overlaying the RNA 6000 ladder onto the electropherogram by holding down the control key while using the mouse to click on the ladder lane in the small gel-like image. The figure shows overlaid electropherograms of bovine lung mRNA, 250 ng/  $\mu$ l, and the RNA 6000 ladder. The ladder contains six fragments of sizes 200, 400, 1000, 2000, 4000 and 6000 nucleotides. The relatively smooth character of the broad bovine lung mRNA peak is typical of a high quality mRNA sample free of ribosomal RNA contamination.







Fragment	Name	Start Time(secs)	End Time(secs)	Area	% of total Area
1	rRNA	29.50	30.35	2.40	13.42
2	rRNA	33.20	34.35	1.66	9.29

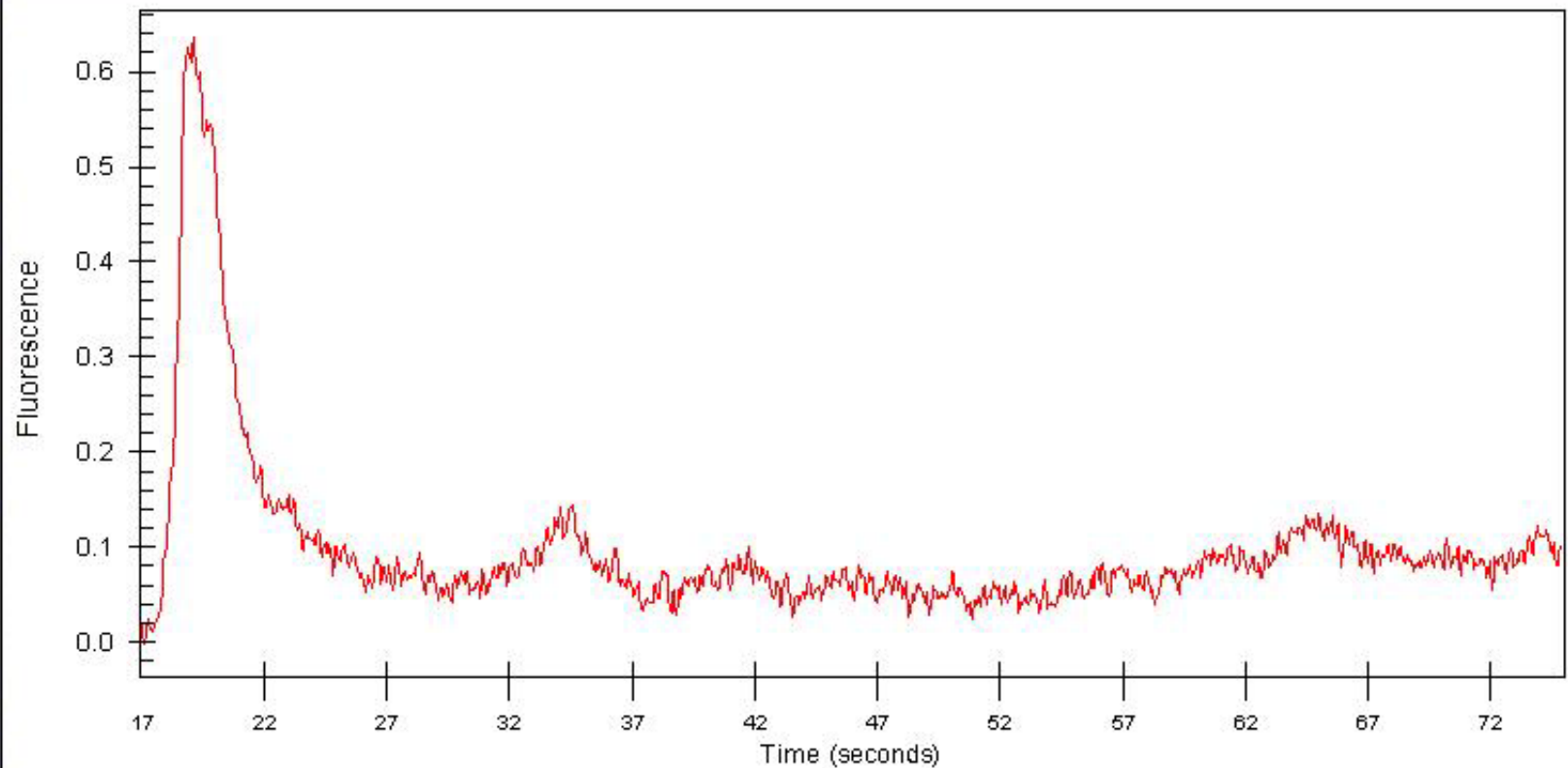
Sample Settings RNA Results Errors

Corrected RNA Area **17.88**

RNA Concentration **29.28 ng/ul**

rRNA Contamination **22.71 %**

## SSBM-V-DM



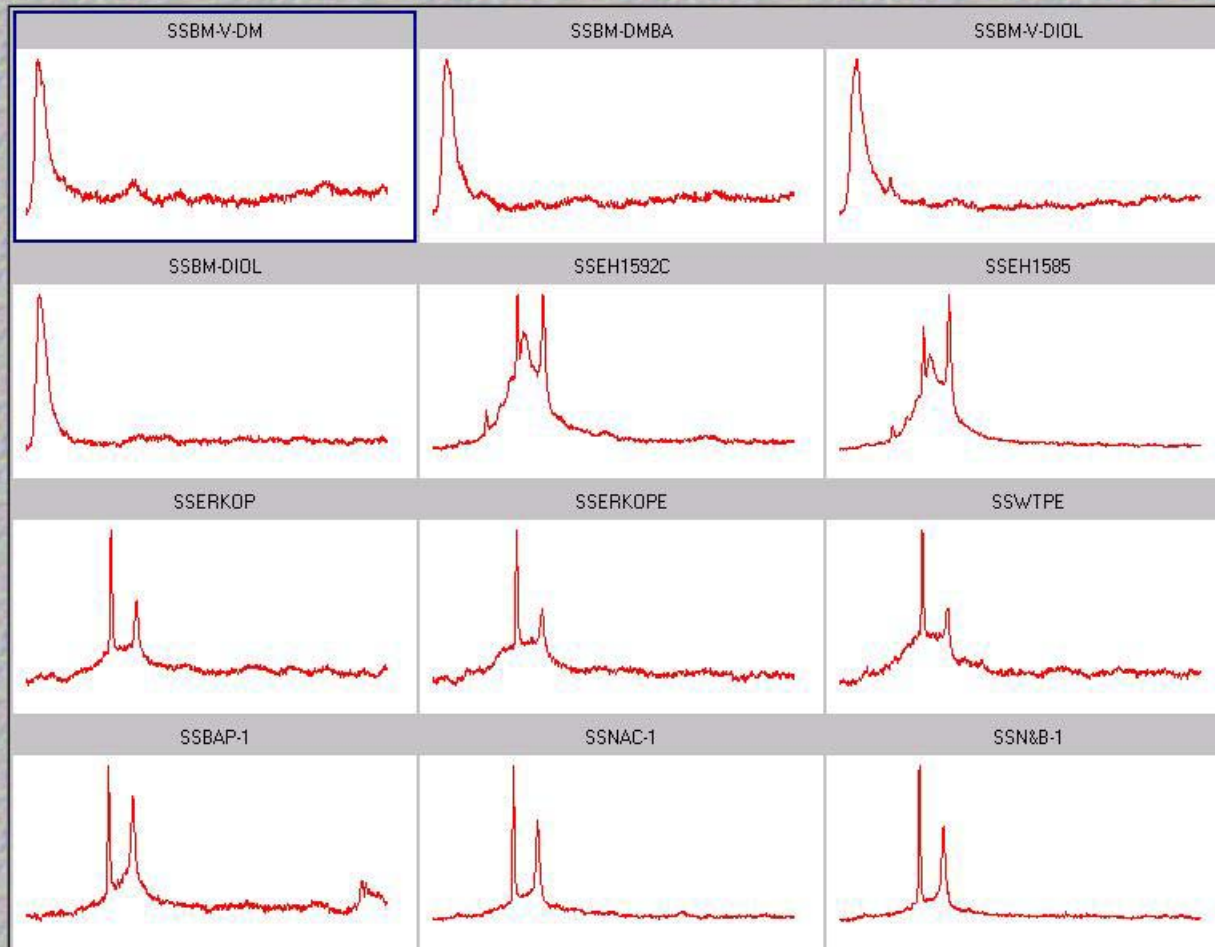
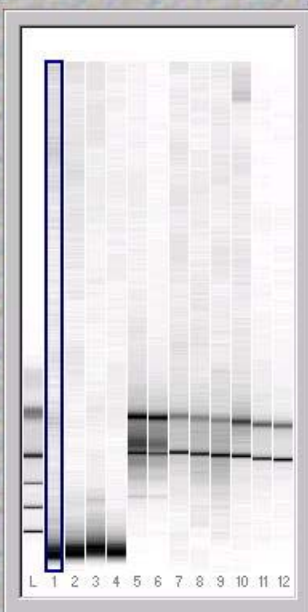
Fragment	Name	Start Time(secs)	End Time(secs)	Area	% of total Area	Sample	Settings	RNA	Results	Errors	
						Corrected RNA Area					3.64
						RNA Concentration					5.97 ng/ul
						rRNA Contamination					0.00 %



Start...

Data File: 2001165ah\_00610\_2001-05-16\_16-19-53  
Read: 5/16/2001,4:19:53 PM

Assay: mRNA



# How should I submit samples?

- First, consider a pilot RNA prep
- Follow the instructions on the web page:
  - Gel and quantitation
  - Label tubes and sheet the same way
  - Notify us in advance of submission
  - Deliver samples on dry ice to a person
  - Label form neatly

<http://dir.niehs.nih.gov/microarray>

Protocols here- check date

Sample submission form

Previous user's group meetings

## Technical Staff:

**Jeff Tucker**- bioengineer

**Astrid Haugen**- validation/special tox projects

**Sherry Grissom**-human, yeast, mouse basic studies

**Danica Ducharme**-robotics/ printing

Stella Sieber

Neysa Garner/Tomo Oshimura-STEPS

Jennifer Collins-web page

Acknowledge and Thanks to Julie Foley